TECH CENTER 1000

SEQUENCE LISTING

Evans, Adam
Henner, William D.

<120> HER-2 BINDING ANTAGONISTS

<130> 49321-16

JUL 1 6 2001

<140> US \Q9/506,079

<141> 2000 \ 01-19

<150> US 09/234,208

<151> 1999-01-20

<160> 10

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<211> 79

<212> PRT

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<223> Applicants herein disclose Thr and Ser sequence variants at this position

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<223> Applicants herein disclose Leu and Pro sequence variants at this position

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 $<\!223\!>$ Applicants herein disclose Gly, Asp, Ala and Val sequence variants at this position

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 $\!<\!223\!>$ Applicants herein disclose Leu and Ile sequence variants at this position

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<223> Applicants herein disclose Pro and Arg sequence variants at this position

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Arg Xaa Gln Pro Xaa Pro Ala His Pro Val Leu Ser Phe Leu Arg Pro 20 25 30

Ser Trp Asp Xaa Val Ser Ala Phe Tyr Ser Leu Pro Leu Ala Pro Leu 35 40 45

Ser Pro Thr Ser Val Xaa Ile Ser Pro Val Ser Val Gly Arg Gly Xaa 50 55 60

Asp Pro Asp Ala His Val Ala Val Xaa Leu Ser Arg Tyr Glu Gly
65 70 75

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<223> Applicants herein disclose Leu and Pro sequence variants at this position

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<223> Applicants herein disclose Gly, Asp, Ala and Val sequence variants at this position

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<223> Applicants herein disclose Leu and Ile sequence variants at this position

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<222> 394

<223> Applicants herein disclose Pro and Arg sequence variants at this position

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<223> Applicants herein disclose Pro and Leu sequence variants at this position

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<223> Applicants herein disclose Asp and Asn sequence variants at this position

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Met Glu Leu Ala Ala Leu Cys Arg Trp Gly Leu Leu Ala Leu Leu Pro Pro Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr Asp Cys Lys Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val Gln Gly Tyr Val Leu Cys Ala His Asn Gln Val Arg Gln Val Pro Leu Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Arg Arg Thr Thr Pro Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser Leu Thr Glu Cys Leu Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys His Pro Cys Ser Pro Cys Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys Ala Arq Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val Thr Tyr Asn Thr Asp Thr Phe Glu Ser Cys Pro Asn Pro Glu Gly Arg Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn Lys Leu Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys Pro Cys Ala Arq Gly Xaa His Ser Xaa Xaa Pro Arg Pro Ala Ala Val Pro Val Pro Xaa Arg Xaa Gln Pro Xaa Pro Ala His Pro Val Leu Ser Phe Leu Arg Pro Ser Trp Asp Xaa Val Ser Ala Phe Tyr Ser Leu Pro

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380
                         375
    370
Leu Ala Pro Leu Asp Pro Thr Ser Val Xaa Ile Ser Pro Val Ser Val
                                         395
                    390
Gly Arg Gly Xaa Asp Pro Asp Ala His Val Ala Val Xaa Leu Ser Arg
                                                          415
                405
                                     410
Tyr Glu Gly
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tccggcagaa atgccaggct cc 22
<210> 5
<211> 22
<212> DNA
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aacacagcgg tgtgagaagt gc 22
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ttcacactgg cacgtccaga cc 22
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Gly Xaa His Ser Xaa Xaa Pro Arg Pro Ala Ala Val Pro Val Pro
                                                          15
                                     10
                 5
cwg cgc atr cag cct gnc cca gcc cac cct gtc cta tcc ttc ctc
Xaa Arg Xaa Gln Pro Xaa Pro Ala His Pro Val Leu Ser Phe Leu
                                     25
                                                          30
                20
aga ccc tct tgg gac mta gtc tct gcc ttc tac tct cta ccc ctg 135
Arg Pro Ser Trp Asp Xaa Val Ser Ala Phe Tyr Ser Leu Pro Leu
                                                          45
                                     40
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			aca Thr						180
 		 _	cct Pro	_	-				225
 tat Tvr	_	 tga							240